UNITED STATES PATENT AND TRADEMARK OFFICE

CERTIFICATE OF CORRECTION

PATENT NO. : 6,994,857 B2
APPLICATION NO. : 09/833041
DATED : February 7, 2006
INVENTOR(S) : Craig A. Rosen and William A. Haseltine

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

Title page item (60), (Related U.S. Application Date) of the title page, delete the text beginning with "Provisional application No. 60/229,358" to and ending with "provisional application No. 60/256,931, filed on Dec. 1, 2000."

On page 7, column 2, in the 8th reference, delete the text beginning with "Hershfield, M.S., et al.," to and ending "7185-7189 (1991)" and insert -- Hochuli, E., "Interferon Immunogenicity: Technical Evaluation of Interferon-α2a," *Journal of Interferon and Cytokine Research* 17:S15-S21 (1997). --

On page 10, column 2, after the 9th reference (Nilsson, J., et al.), insert -- Nilsson, J. et al., "Heat-Mediated Activation of Affinity-Immobilized Taq DNA Polymerase," *BioTechniques* 22:744-751 (1997). --

Title page item (57) (ABSTRACT) of the title page, "disordrs" should read -- disorders--.

In the Specification:

Col. 25 (Table 1), row HLDOU18, column Exemplary Identifier, "SEQ ID NO:73" should read -- SEQ ID NO:74 --.

Col.27 (Table 1), row HWACB86, column Exemplary Identifier, "SEQ ID NO 74" should read -- SEQ ID NO:75 --.

Col. 27 (Table 1), row HCEGG08, column Exemplary Identifier, "SEQ ID NO:75" should read -- SEQ ID NO:76 --.

Col. 29 (Table 1), row HWHGZ51, column Exemplary Identifier, "SEQ ID NO:76" should read -- SEQ ID NO:77 --.

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PATENT NO. : 6,994,857 B2
APPLICATION NO. : 09/833041
DATED : February 7, 2006
INVENTOR(S) : DCraig A. Rosen and William A. Haseltine

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

Col. 29 (Table 1), row HDTAI21, column Exemplary Identifer, "SEQ ID NO: 77" should read -- SEQ ID NO: 78 --.

Col. 29 (Table 1), row HCNCA73, column Exemplary Identifer, "SEQ ID NO: 78" should read -- SEQ ID NO: 79 --.

Col. 29 (Table 1), row HNHFE71, column Exemplary Identifer, "SEQ ID NO: 79" should read -- SEQ ID NO: 80--.

Col. 62, lines 38-39, "(SEQ ID NO:36)" should read -- (SEQ ID NO:72) --.

Col. 215, line 8, "(SEQ ID NO:36)" should read -- (SEQ ID NO:81) --.

Col. 236, line 42, "(SEQ ID NO:37)" should read -- (SEQ ID NO:82) --.

Col. 237, line 47,"(SEQ ID NO:38)" should read -- (SEQ ID NO:83) --.
Col. 237, lines 53-54, "(SEQ ID NO:39)" should read -- (SEQ ID NO:84) --.
Col. 237, line 63, "(SEQ ID NO:40)" should read -- (SEQ ID NO:85) --.

Col. 240, line 55, "(SEQ ID NO:41)" should read -- (SEQ ID NO:86) --.
Col. 240, line 58, "(SEQ ID NO:42)" should read -- (SEQ ID NO:87) --.

Col. 243, line 9,"(SEQ ID NO:43)" should read -- (SEQ ID NO:88) --.
Col. 243, line 14,"(SEQ ID NO:44)" should read -- (SEQ ID NO:89) --.
Col. 243, lines 17-18, "(SEQ ID NO:39)" should read -- (SEQ ID NO:84) --.
Col. 243, line 28, "(SEQ ID NO:45)" should read -- (SEQ ID NO:90) --.

In the Sequence Listing:

Delete the Sequence Listing beginning in Col. 263, with the text "<160> NUMBER OF SEQ ID NOS:79" to and ending " **Pro Thr Ser Cys Ser Arg Cys** "
165

In Col. 313 and insert the following Sequence Listing:
--

<160> NUMBER OF SEQ ID NOS: 90

<210> 1
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer useful to clone human growth hormone cDNA

<400> 1
cccaagaatt cccttatcca ggc 23

<210> 2
<211> 33
<212> DNA
<213> Artificial Sequence
<220>
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<223> primer useful to clone human growth hormone cDNA

<400> 2
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<210> 3
<211> 16
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_structure
<223> synthetic oligonucleotide used to join DNA fragments
with non-cohesive ends.

<400> 3
gataaagatt cccaac 16

<210> 4
<211> 17
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_structure
<223> synthetic oligonucleotide used to join DNA fragments
with non-cohesive ends.

<400> 4
aattgttggg aatcttt 17

<210> 5
<211> 17
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_structure

<223> synthetic oligonucleotide used to join DNA fragments
with non-cohesive ends.

<400> 5
ttaggcttat tcccaac 17

<210> 6
<211> 18
<212> DNA
<213> Artificial Sequence
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<221> misc_structure
<223> synthetic oligonucleotide used to join DNA fragments
with non-cohesive ends.

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<221> SITE
<222> 20)..(24)
<223> first 5 amino acids of mature human serum albumin

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1 5 10 15

Ile Ser Ala Asp Ala His Lys Ser
20

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<212> DNA
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fragments with non-cohesive ends.

<400> 8
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<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

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<213> Artificial Sequence
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<221> misc_structure
<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

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<210> 11
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<213> Artificial Sequence
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<400> 11
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<213> Artificial Sequence
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<400> 13
ttaggcttag gtggcggtgg atccggcggt ggtggatctt tcccaac 47

<210> 14
<211> 48
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<213> Artificial Sequence
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fragments with non-cohesive ends.

<400> 14
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<210> 15
<211> 62
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<220>
<221> misc_structure
<223> synthetic oligonucleotide used to join DNA
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ac 62

<210> 16
<211> 63
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_structure
<223> synthetic oligonucleotide used to join DNA
fragments with non-cohesive ends.

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aattgttggg aaggatccac cgccaccaga tccgccgcca ccagatccac caccgcctaa 60

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gcc                                                                    63


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<211> 1782
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<213> Homo sapiens
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gaa aat ttc aaa gcc ttg gtg ttg att gcc ttt gct cag tat ctt cag   96
Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20                  25                  30

cag tgt cca ttt gaa gat cat gta aaa tta gtg aat gaa gta act gaa   144
Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
         35                  40                  45

ttt gca aaa aca tgt gtt gct gat gag tca gct gaa aat tgt gac aaa   192
Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
     50                  55                  60

tca ctt cat acc ctt ttt gga gac aaa tta tgc aca gtt gca act ctt   240
Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
 65                  70                  75                  80

cgt gaa acc tat ggt gaa atg gct gac tgc tgt gca aaa caa gaa cct   288
Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

gag aga aat gaa tgc ttc ttg caa cac aaa gat gac aac cca aac ctc   336
Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

ccc cga ttg gtg aga cca gag gtt gat gtg atg tgc act gct ttt cat   384
Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

gac aat gaa gag aca ttt ttg aaa aaa tac tta tat gaa att gcc aga   432
Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

aga cat cct tac ttt tat gcc ccg gaa ctc ctt ttc ttt gct aaa agg   480
Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160
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tat aaa gct gct ttt aca gaa tgt tgc caa gct gct gat aaa gct gcc   528
Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

tgc ctg ttg cca aag ctc gat gaa ctt cgg gat gaa ggg aag gct tcg   576
Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

tct gcc aaa cag aga ctc aaa tgt gcc agt ctc caa aaa ttt gga gaa   624
Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

aga gct ttc aaa gca tgg gca gtg gct cgc ctg agc cag aga ttt ccc   672
Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
    210                 215                 220

aaa gct gag ttt gca gaa gtt tcc aag tta gtg aca gat ctt acc aaa   720
Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225                 230                 235                 240

gtc cac acg gaa tgc tgc cat gga gat ctg ctt gaa tgt gct gat gac   768
Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

agg gcg gac ctt gcc aag tat atc tgt gaa aat cag gat tcg atc tcc   816
Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

agt aaa ctg aag gaa tgc tgt gaa aaa cct ctg ttg gaa aaa tcc cac   864
Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

tgc att gcc gaa gtg gaa aat gat gag atg cct gct gac ttg cct tca   912
Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

tta gct gct gat ttt gtt gaa agt aag gat gtt tgc aaa aac tat gct   960
Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

gag gca aag gat gtc ttc ctg ggc atg ttt ttg tat gaa tat gca aga   1008
Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

agg cat cct gat tac tct gtc gtg ctg ctg ctg aga ctt gcc aag aca   1056
Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

tat gaa acc act cta gag aag tgc tgt gcc gct gca gat cct cat gaa   1104
Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365
```

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tgc tat gcc aaa gtg ttc gat gaa ttt aaa cct ctt gtg gaa gag cct  1152
Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

cag aat tta atc aaa caa aac tgt gag ctt ttt gag cag ctt gga gag  1200
Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

tac aaa ttc cag aat gcg cta tta gtt cgt tac acc aag aaa gta ccc  1248
Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

caa gtg tca act cca act ctt gta gag gtc tca aga aac cta gga aaa  1296
Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

gtg ggc agc aaa tgt tgt aaa cat cct gaa gca aaa aga atg ccc tgt  1344
Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

gca gaa gac tat cta tcc gtg gtc ctg aac cag tta tgt gtg ttg cat  1392
Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

gag aaa acg cca gta agt gac aga gtc aca aaa tgc tgc aca gag tcc  1440
Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

ttg gtg aac agg cga cca tgc ttt tca gct ctg gaa gtc gat gaa aca  1488
Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

tac gtt ccc aaa gag ttt aat gct gaa aca ttc acc ttc cat gca gat  1536
Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

ata tgc aca ctt tct gag aag gag aga caa atc aag aaa caa act gca  1584
Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

ctt gtt gag ctt gtg aaa cac aag ccc aag gca aca aaa gag caa ctg  1632
Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

aaa gct gtt atg gat gat ttc gca gct ttt gta gag aag tgc tgc aag  1680
Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

gct gac gat aag gag acc tgc ttt gcc gag gag ggt aaa aaa ctt gtt  1728
Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575
```

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gct gca agt caa gct gcc tta ggc tta taacatctac atttaaaagc atctcag 1782
Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585

<210> 18
<211> 585
<212> PRT
<213> Homo Sapiens

<400> 18
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
  1               5                  10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
             20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
         35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
     50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
 65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                 85                  90                  95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
    210                 215                 220
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Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225                 230                 235                 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495
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Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
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Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
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Ala Ala Ser Gln Ala Ala Leu Gly Leu
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<223> primer used to generate XhoI and ClaI site in pPPC0006

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<223> primer used in generation XhoI and ClaI

site in pPPC0006

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<210> 24
<211> 60
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<210> 25
<211> 32
<212> DNA
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<220>
<221> primer_bind
<223> forward primer useful for generation of albumin

fusion protein in which the albumin moiety is N-terminal of the Therapeutic Protein

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<223> reverse primer useful for generation of albumin fusion protein in which the albumin moiety is N-terminal of the Therapeutic Protein

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<223> forward primer useful for generation of albumin fusion protein in which the albumin moiety is c-terminal of the Therapeutic Protein

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<400> 27
aggagcgtcg acaaaagann nnnnnnnnnn nnn 33

<210> 28
<211> 52
<212> DNA

<213> Artificial Sequence
<220>
<221> primer_bind
<223> reverse primer useful for generation of albumin fusion protein in which the albumin moiety is c-terminal of the Therapeutic Protein

<220>
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<400> 28
ctttaaatcg atgagcaacc tcactcttgt gtgcatcnnn nnnnnnnnnn nn 52

<210> 29
<211> 24
<212> PRT
<213> Artificial Sequence
<220>
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<223> signal peptide of natural human serum albumin protein

<400> 29
Met Lys Trp Val Ser Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Arg Ser Leu Asp Lys Arg
20

<210> 30
<211> 114
<212> DNA

<213> Artificial Sequence

<220>
<221> primer_bind
<223> forward primer useful for generation of PC4:HSA albumin fusion VECTOR

<220>
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<222> (5)..(10)
<223> BamHI retsriction site

<220>
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<222> (11)..(16)
<223> Hind III retsriction site

<220>
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<222> (17)..(27)
<223> Kozak sequence

<220>
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<222> (25)..(97)
<223> cds natural signal sequence of human serum albumin

<220>
<221> misc_feature
<222> (75)..(81)
<223> XhoI restriction site

<220>
<221> misc_feature
<222> (98)..(114)
<223> cds first six amino acids of human serum albumin

<400> 30
tcagggatcc aagcttccgc caccatgaag tgggtaacct ttatttccct cttttttctc 60

tttagctcgg cttactcgag gggtgtgttt cgtcgagatg cacacaagag tgag 114

<210> 31
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
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<223> reverse primer useful for generation of PC4:HSA albumin fusion VECTOR

<220>
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<220>
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<222> (12)..(17)
<223> EcoRI restriction site

<220>
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<222> (15)..(17)
<223> reverse complement of stop codon

<220>
<221> misc_feature
<222> (18)..(25)
<223> AscI restriction site

<220>
<221> misc_feature
<222> (18)..(43)
<223> reverse complement of DNA sequence encoding last 9 amino acids

<400> 31
gcagcggtac cgaattcggc gcgccttata agcctaaggc agc 43

<210> 32
<211> 46
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> forward primer useful for inserting Therapeutic protein into pC4:HSA vector

<220>
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<223> n equals a,t,g, or c

<400> 32
ccgccgctcg aggggtgtgt ttcgtcgann nnnnnnnnnn nnnnnn 46

<210> 33
<211> 55
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> reverse primer useful for inserting Therapeutic protein into pC4:HSA vector

<220>
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<222> (38)
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<400> 33
agtcccatcg atgagcaacc tcactcttgt gtgcatcnnn nnnnnnnnnn nnnnn 55

<210> 34
<211> 17
<212> PRT
<213> Artificial Sequence
<220>
<221> signal
<223> Stanniocalcin signal peptide

<400> 34
Met Leu Gln Asn Ser Ala Val Leu Leu Leu Val Ile Ser Ala Ser
1 5 10 15

Ala

<210> 35
<211> 22
<212> PRT
<213> Artificial Sequence
<220>
<221> signal
<223> Synthetic signal peptide

<400> 35
Met Pro Thr Trp Ala Trp Trp Leu Phe Leu Val Leu Leu Leu Ala Leu
1 5 10 15

Trp Ala Pro Ala Arg Gly
20

<210> 36
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for amplifying human VH domains

<400> 36
caggtgcagc tggtgcagtc tgg 23

<210> 37
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for amplifying human VH domains

<400> 37
caggtcaact taagggagtc tgg 23

<210> 38
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for amplifying human VH domains

<400> 38
gaggtgcagc tggtggagtc tgg 23

<210> 39
<211> 23
<212> DNA
<213> Artificial Sequence
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<221>primer_bind
<223>Degenerate VH forward primer useful for amplifying human VH domains

<400> 39

caggtgcagc tgcaggagtc ggg 23

<210> 40
<211> 23
<212> DNA
<213> Artificial Sequence
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<221>primer_bind
<223>Degenerate VH forward primer useful for amplifying human VH domains

<400> 40
gaggtgcagc tgttgcagtc tgc 23

<210> 41
<211> 23
<212> DNA
<213> Artificial Sequen
<220>
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<400> 41
caggtacagc tgcagcagtc agg 23

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence
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<223>Degenerate JH reverse primer useful for amplifying human VH domains

<400> 42
tgaggagacg gtgaccaggg tgcc 24

<210> 43
<211> 24
<212> DNA
<213> Artificial Sequence
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<221>primer_bind
<223>Degenerate JH reverse primer useful for amplifying human VH domains

<400> 43
tgaagagacg gtgaccattg tccc 24

<210> 44

<211> 24
<212> DNA
<213> Artificial Sequence
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<221>primer_bind
<223>Degenerate JH reverse primer useful for
amplifying human VH domains

<400> 44
tgaggagacg gtgaccaggg ttcc 24

<210> 45
<211> 24
<212> DNA
<213> Artificial Sequence
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<221>primer_bind
<223>Degenerate JH reverse primer useful for
amplifying human VH domains

<400> 45
tgaggagacg gtgaccgtgg tccc 24

<210> 46
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Vkappa forward primer useful for
amplifying human VL domains

<400> 46
gacatccaga tgacccagtc tcc 23

<210> 47
<211> 23
<212> DNA
<213> Artificial Sequence
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<221>primer_bind
<223>Degenerate Vkappa forward primer useful for
amplifying human VL domains

<400> 47
gatgttgtga tgactcagtc tcc 23

<210> 48
<211> 23
<212> DNA
<213> Artificial Sequence
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<221>primer_bind
<223>Degenerate Vkappa forward primer useful for amplifying human VL domains

<400> 48
gatattgtga tgactcagtc tcc 23

<210> 49
<211> 23
<212> DNA
<213> Artificial Sequence
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<223>Degenerate Vkappa forward primer useful for amplifying human VL domains

<400> 49
gaaattgtgt tgacgcagtc tcc 23

<210> 50
<211> 23
<212> DNA
<213> Artificial Sequence
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<223>Degenerate Vkappa forward primer useful for amplifying human VL domains

<400> 50
gacatcgtga tgacccagtc tcc 23

<210> 51
<211> 23
<212> DNA
<213> Artificial Sequence
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<223>Degenerate Vkappa forward primer useful for amplifying human VL domains

<400> 51
gaaacgacac tcacgcagtc tcc 23

<210> 52
<211> 23
<212> DNA
<213> Artificial Sequence
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<400> 52
gaaattgtgc tgactcagtc tcc 23

<210> 53
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Vlambda forward primer useful for amplifying human VL domains

<400> 53
cagtctgtgt tgacgcagcc gcc 23

<210> 54
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Vlambda forward primer useful for amplifying human VL domains

<400> 54
cagtctgccc tgactcagcc tgc 23

<210> 55
<211> 23
<212> DNA
<213> Artificial Sequence
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<400> 55
tcctatgtgc tgactcagcc acc 23

<210> 56
<211> 23
<212> DNA
<213> Artificial Sequence
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<400> 56
tcttctgagc tgactcagga ccc 23

<210> 57

<211> 23
<212> DNA
<213> Artificial Sequence
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<221>primer_bind
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amplifying human VL domains

<400> 57
cacgttatac tgactcaacc gcc 23

<210> 58
<211> 23
<212> DNA
<213> Artificial Sequence
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<223>Degenerate Vlambda forward primer useful for
amplifying human VL domains

<400> 58
caggctgtgc tcactcagcc gtc 23

<210> 59
<211> 23
<212> DNA
<213> Artificial Sequence
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amplifying human VL domains

<400> 59
aattttatgc tgactcagcc cca 23

<210> 60
<211> 24
<212> DNA
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amplifying human VL domains

<400> 60
acgtttgatt tccaccttgg tccc 24

<210> 61
<211> 24
<212> DNA
<213> Artificial Sequence
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<400> 61
acgtttgatc tccagcttgg tccc 24

<210> 62
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
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<400> 62
acgtttgata tccactttgg tccc 24

<210> 63
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Jkappa reverse primer useful for amplifying human VL domains

<400> 63
acgtttgatc tccaccttgg tccc 24

<210> 64
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Jkappa reverse primer useful for amplifying human VL domains

<400> 64
acgtttaatc tccagtcgtg tccc 24

<210> 65
<211> 23
<212> DNA
<213> Artificial Sequence
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<221>primer_bind
<223>Degenerate Jlambda reverse primer useful for amplifying human VL domains

<400> 65
cagtctgtgt tgacgcagcc gcc 23

<210> 66
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Jlambda reverse primer useful for amplifying human VL domains

<400> 66
cagtctgccc tgactcagcc tgc 23

<210> 67
<211> 23
<212> DNA
<213> Artificial Sequence
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<223>Degenerate Jlambda reverse primer useful for amplifying human VL domains

<400> 67
tcctatgtgc tgactcagcc acc 23

<210> 68
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
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<400> 68
tcttctgagc tgactcagga ccc 23

<210> 69
<211> 23
<212> DNA
<213> Artificial Sequence
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<221>primer_bind
<223>Degenerate Jlambda reverse primer useful for amplifying human VL domains

<400> 69
cacgttatac tgactcaacc gcc 23

<210> 70

<211> 23
<212> DNA
<213> Artificial Sequence
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amplifying human VL domains

<400> 70
caggctgtgc tcactcagcc gtc 23

<210> 71
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Jlambda reverse primer useful for
amplifying human VL domains

<400> 71
aattttatgc tgactcagcc cca 23

<210> 72
<211> 15
<212> PRT
<213> Artificial Sequence
<220>
<221>turn
<223>Linker peptide that may be used to join VH
and VL domains in an scFv.

<400> 72
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 73
<211> 23
<212> PRT
<213> Homo sapiens

<400> 73
Cys Cys Cys Ala Ala Gly Ala Ala Thr Thr Cys Cys Cys Thr Thr Ala
1 5 10 15

Thr Cys Cys Ala Gly Gly Cys
20

<210> 74
<211> 429
<212> PRT

<213> Homo sapiens

<400> 74

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Met Cys Pro Gly Ala Leu Trp Val Ala Leu Pro Leu Leu Ser Leu Leu
 1               5                  10                  15

Ala Gly Ser Leu Gln Gly Lys Pro Leu Gln Ser Trp Gly Arg Gly Ser
            20                  25                  30

Ala Gly Gly Asn Ala His Ser Pro Leu Gly Val Pro Gly Gly Gly Leu
        35                  40                  45

Pro Glu His Thr Phe Asn Leu Lys Met Phe Leu Glu Asn Val Lys Val
    50                  55                  60

Asp Phe Leu Arg Ser Leu Asn Leu Ser Gly Val Pro Ser Gln Asp Lys
65                  70                  75                  80

Thr Arg Val Glu Pro Pro Gln Tyr Met Ile Asp Leu Tyr Asn Arg Tyr
                85                  90                  95

Thr Ser Asp Lys Ser Thr Thr Pro Ala Ser Asn Ile Val Arg Ser Phe
            100                 105                 110

Ser Met Glu Asp Ala Ile Ser Ile Thr Ala Thr Glu Asp Phe Pro Phe
        115                 120                 125

Gln Lys His Ile Leu Leu Phe Asn Ile Ser Ile Pro Arg His Glu Gln
    130                 135                 140

Ile Thr Arg Ala Glu Leu Arg Leu Tyr Val Ser Cys Gln Asn His Val
145                 150                 155                 160

Asp Pro Ser His Asp Leu Lys Gly Ser Val Val Ile Tyr Asp Val Leu
                165                 170                 175

Asp Gly Thr Asp Ala Trp Asp Ser Ala Thr Glu Thr Lys Thr Phe Leu
            180                 185                 190

Val Ser Gln Asp Ile Gln Asp Glu Gly Trp Glu Thr Leu Glu Val Ser
        195                 200                 205

Ser Ala Val Lys Arg Trp Val Arg Ser Asp Ser Thr Lys Ser Lys Asn
    210                 215                 220

Lys Leu Glu Val Thr Val Glu Ser His Arg Lys Gly Cys Asp Thr Leu
225                 230                 235                 240

Asp Ile Ser Val Pro Pro Gly Ser Arg Asn Leu Pro Phe Phe Val Val
                245                 250                 255
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Phe Ser Asn Asp His Ser Ser Gly Thr Lys Glu Thr Arg Leu Glu Leu
            260                 265                 270

Arg Glu Met Ile Ser His Glu Gln Glu Ser Val Leu Lys Lys Leu Ser
        275                 280                 285

Lys Asp Gly Ser Thr Glu Ala Gly Glu Ser Ser His Glu Glu Asp Thr
    290                 295                 300

Asp Gly His Val Ala Ala Gly Ser Thr Leu Ala Arg Arg Lys Arg Ser
305                 310                 315                 320

Ala Gly Ala Gly Ser His Cys Gln Lys Thr Ser Leu Arg Val Asn Phe
                325                 330                 335

Glu Asp Ile Gly Trp Asp Ser Trp Ile Ile Ala Pro Lys Glu Tyr Glu
            340                 345                 350

Ala Tyr Glu Cys Lys Gly Gly Cys Phe Phe Pro Leu Ala Asp Asp Val
        355                 360                 365

Thr Pro Thr Lys His Ala Ile Val Gln Thr Leu Val His Leu Lys Phe
    370                 375                 380

Pro Thr Lys Val Gly Lys Ala Cys Cys Val Pro Thr Lys Leu Ser Pro
385                 390                 395                 400

Ile Ser Val Leu Tyr Lys Asp Asp Met Gly Val Pro Thr Leu Lys Tyr
                405                 410                 415

His Tyr Glu Gly Met Ser Val Ala Glu Cys Gly Cys Arg
            420                 425

<210> 75
<211> 280
<212> PRT
<213> Homo sapiens

<400> 75
Met Ala Pro Ser Gly Ser Leu Ala Val Pro Leu Ala Val Leu Val Leu
  1                 5                  10                  15

Leu Leu Trp Gly Ala Pro Trp Thr His Gly Arg Arg Ser Asn Val Arg
             20                  25                  30

Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly Asp Trp Met
         35                  40                  45

Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln Asn Leu Gln Pro
     50                  55                  60
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Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp Leu Glu Val Asn Ile
 65                  70                  75                  80

Ala Lys Val Asp Val Thr Glu Gln Pro Gly Leu Ser Gly Arg Phe Ile
                85                  90                  95

Ile Thr Ala Leu Pro Thr Ile Tyr His Cys Lys Asp Gly Glu Phe Arg
            100                 105                 110

Arg Tyr Gln Gly Pro Arg Thr Lys Lys Asp Phe Ile Asn Phe Ile Ser
        115                 120                 125

Asp Lys Glu Trp Lys Ser Ile Glu Pro Val Ser Ser Trp Phe Gly Pro
    130                 135                 140

Gly Ser Val Leu Met Ser Ser Met Ser Ala Leu Phe Gln Leu Ser Met
145                 150                 155                 160

Trp Ile Arg Thr Cys His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro
                165                 170                 175

Val Trp Gly Ser Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly
            180                 185                 190

Leu Leu Leu Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro
        195                 200                 205

Ser Lys Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu
    210                 215                 220

Leu Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu
225                 230                 235                 240

Ala Asp Glu Glu Asp Val Ser Glu Glu Glu Ala Glu Ser Lys Glu Gly
                245                 250                 255

Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser Leu Gly
            260                 265                 270

Pro Ser Leu Ala Thr Asp Lys Ser
        275                 280
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<210> 76
<211> 112
<212> PRT
<213> Homo sapiens

<400> 76

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Met Phe Trp Val Met Glu Thr Ala Lys Pro Pro Val Ser Glu Asp Ser
  1               5                  10                  15
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Phe Arg Leu Pro Arg Lys Trp Gly Trp Arg Thr Glu Ala Thr Ala Pro
            20                  25                  30

His Ala Pro Val Pro Gln Ser Ile Cys Pro Arg Tyr Thr Ser Pro Cys
        35                  40                  45

Ala Pro His Asp Cys Gly Ser Gln Thr Val Gln Gly Asn Ser Leu Ser
    50                  55                  60

Leu Phe Tyr Thr Leu Ser His Lys Ala Pro Gln Leu Pro His Arg Val
65                  70                  75                  80

Pro Ala Pro Leu Phe Cys Lys Tyr Val Lys Arg Lys Lys Cys Lys Arg
                85                  90                  95

Trp Ser Leu Gly Trp Ser Ser Ser Leu Gln Leu Arg Leu Leu Thr Met
            100                 105                 110

<210> 77
<211> 346
<212> PRT
<213> Homo sapiens

<400> 77
Met Asp Pro Ala Arg Lys Ala Gly Ala Gln Ala Met Ile Trp Thr Ala
 1               5                  10                  15

Gly Trp Leu Leu Leu Leu Leu Leu Arg Gly Gly Ala Gln Ala Leu Glu
            20                  25                  30

Cys Tyr Ser Cys Val Gln Lys Ala Asp Asp Gly Cys Ser Pro Asn Lys
        35                  40                  45

Met Lys Thr Val Lys Cys Ala Pro Gly Val Asp Val Cys Thr Glu Ala
    50                  55                  60

Val Gly Ala Val Glu Thr Ile His Gly Gln Phe Ser Leu Ala Val Arg
65                  70                  75                  80

Gly Cys Gly Ser Gly Leu Pro Gly Lys Asn Asp Arg Gly Leu Asp Leu
                85                  90                  95

His Gly Leu Leu Ala Phe Ile Gln Leu Gln Gln Cys Ala Gln Asp Arg
            100                 105                 110

Cys Asn Ala Lys Leu Asn Leu Thr Ser Arg Ala Leu Asp Pro Ala Gly
        115                 120                 125

Asn Glu Ser Ala Tyr Pro Pro Asn Gly Val Glu Cys Tyr Ser Cys Val
    130                 135                 140
```

```
Gly Leu Ser Arg Glu Ala Cys Gln Gly Thr Ser Pro Pro Val Val Ser
145                 150                 155                 160

Cys Tyr Asn Ala Ser Asp His Val Tyr Lys Gly Cys Phe Asp Gly Asn
                165                 170                 175

Val Thr Leu Thr Ala Ala Asn Val Thr Val Ser Leu Pro Val Arg Gly
            180                 185                 190

Cys Val Gln Asp Glu Phe Cys Thr Arg Asp Gly Val Thr Gly Pro Gly
        195                 200                 205

Phe Thr Leu Ser Gly Ser Cys Cys Gln Gly Ser Arg Cys Asn Ser Asp
    210                 215                 220

Leu Arg Asn Lys Thr Tyr Phe Ser Pro Arg Ile Pro Pro Leu Val Arg
225                 230                 235                 240

Leu Pro Pro Pro Glu Pro Thr Thr Val Ala Ser Thr Thr Ser Val Thr
                245                 250                 255

Thr Ser Thr Ser Ala Pro Val Arg Pro Thr Ser Thr Thr Lys Pro Met
            260                 265                 270

Pro Ala Pro Thr Ser Gln Thr Pro Arg Gln Gly Val Glu His Glu Ala
        275                 280                 285

Ser Arg Asp Glu Glu Pro Arg Leu Thr Gly Gly Ala Ala Gly His Gln
    290                 295                 300

Asp Arg Ser Asn Ser Gly Gln Tyr Pro Ala Lys Gly Gly Pro Gln Gln
305                 310                 315                 320

Pro His Asn Lys Gly Cys Val Ala Pro Thr Ala Gly Leu Ala Ala Leu
                325                 330                 335

Leu Leu Ala Val Ala Ala Gly Val Leu Leu
            340                 345

<210> 78
<211> 272
<212> PRT
<213> Homo sapiens

<400> 78
Met Lys Gly Lys Lys Gly Ile Val Ala Ala Ser Gly Ser Glu Thr Glu
  1               5                  10                  15

Asp Glu Asp Ser Met Asp Ile Pro Leu Asp Leu Ser Ser Ser Ala Gly
            20                  25                  30
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```
Ser Gly Lys Arg Arg Arg Arg Gly Asn Leu Pro Lys Glu Ser Val Gln
          35                  40                  45

Ile Leu Arg Asp Trp Leu Tyr Glu His Arg Tyr Asn Ala Tyr Pro Ser
      50                  55                  60

Glu Gln Glu Lys Ala Leu Leu Ser Gln Gln Thr His Leu Ser Thr Leu
 65                  70                  75                  80

Gln Val Cys Asn Trp Phe Ile Asn Ala Arg Arg Arg Leu Leu Pro Asp
                 85                  90                  95

Met Leu Arg Lys Asp Gly Lys Asp Pro Asn Gln Phe Thr Ile Ser Arg
            100                 105                 110

Arg Gly Ala Lys Ile Ser Glu Thr Ser Ser Val Glu Ser Val Met Gly
        115                 120                 125

Ile Lys Asn Phe Met Pro Ala Leu Glu Glu Thr Pro Phe His Ser Cys
    130                 135                 140

Thr Ala Gly Pro Asn Pro Thr Leu Gly Arg Pro Leu Ser Pro Lys Pro
145                 150                 155                 160

Ser Ser Pro Gly Ser Val Leu Ala Arg Pro Ser Val Ile Cys His Thr
                165                 170                 175

Thr Val Thr Ala Leu Lys Asp Val Pro Phe Ser Leu Cys Gln Ser Val
            180                 185                 190

Gly Val Gly Gln Asn Thr Asp Ile Gln Gln Ile Ala Ala Lys Asn Phe
        195                 200                 205

Thr Asp Thr Ser Leu Met Tyr Pro Glu Asp Thr Cys Lys Ser Gly Pro
    210                 215                 220

Ser Thr Asn Thr Gln Ser Gly Leu Phe Asn Thr Pro Pro Pro Thr Pro
225                 230                 235                 240

Pro Asp Leu Asn Gln Asp Phe Ser Gly Phe Gln Leu Leu Val Asp Val
                245                 250                 255

Ala Leu Lys Arg Ala Ala Glu Met Glu Leu Gln Ala Lys Leu Thr Ala
            260                 265                 270
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<210> 79
<211> 167
<212> PRT
<213> Homo sapiens

<400> 79
Met Leu Thr Val Ala Leu Leu Ala Leu Leu Cys Ala Ser Ala Ser Gly
1 5 10 15

Asn Ala Ile Gln Ala Arg Ser Ser Ser Tyr Ser Gly Glu Tyr Gly Gly
20 25 30

Gly Gly Gly Lys Arg Phe Ser His Ser Gly Asn Gln Leu Asp Gly Pro
35 40 45

Ile Thr Ala Leu Arg Val Arg Val Asn Thr Tyr Tyr Ile Val Gly Leu
50 55 60

Gln Val Arg Tyr Gly Lys Val Trp Ser Asp Tyr Val Gly Gly Arg Asn
65 70 75 80

Gly Asp Leu Glu Glu Ile Phe Leu His Pro Gly Glu Ser Val Ile Gln
85 90 95

Val Ser Gly Lys Tyr Lys Trp Tyr Leu Lys Lys Leu Val Phe Val Thr
100 105 110

Asp Lys Gly Arg Tyr Leu Ser Phe Gly Lys Asp Ser Gly Thr Ser Phe
115 120 125

Asn Ala Val Pro Leu His Pro Asn Thr Val Leu Arg Phe Ile Ser Gly
130 135 140

Arg Ser Gly Ser Leu Ile Asp Ala Ile Gly Leu His Trp Asp Val Tyr
145 150 155 160

Pro Thr Ser Cys Ser Arg Cys
165

<210> 80
<211> 22
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (22)
<223> Xaa equals stop translation

<400> 80

Met Leu Ala Ala Leu Ala Cys Ser Trp Arg Leu Leu Ser Leu Gly Ala
1 5 10 15

His Ser Gly Arg Ala Xaa
20

<210> 81

<211> 733
<212> DNA
<213> Homo sapiens

<400> 81
gggatccgga gcccaaatct tctgacaaaa ctcacacatg cccaccgtgc ccagcacctg 60

aattcgaggg tgcaccgtca gtcttcctct tccccccaaa acccaaggac accctcatga 120

tctcccggac tcctgaggtc acatgcgtgg tggtggacgt aagccacgaa gaccctgagg 180

tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240

aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300

ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca acccccatcg 360

agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420

catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaaggcttct 480

atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga 540

ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag ctcaccgtgg 600

acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc 660

acaaccacta cacgcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc 720

gactctagag gat

<210> 82
<211> 5
<212> PRT
<213> Artificial sequence
<220>
<221> misc_structure
<223> membrane proximal motif of class 1 cytokine receptors

<220>
<221> misc_feature
<222> (3)
<223> Xaa equals any

<400> 82
Trp Ser Xaa Trp Ser
1 5

<210> 83
<211> 86
<212> DNA

<213> Artificial Sequence
<220>
<221> primer_bind
<223> forward primer useful for generation of a synthetic gamma activation site (GAS) containing promoter element

<400> 83
gcgcctcgag atttccccga aatctagatt tccccgaaat gatttccccg aaatgatttc 60

cccgaaatat ctgccatctc aattag 86

<210> 84
<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> reverse primer useful for generation of a synthetic gamma activation site (GAS) containing promoter element

<400> 84
gcggcaagct ttttgcaaag cctaggc 27

<210> 85
<211> 271
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_feature
<223> Synthetic GAS-SV40 promoter sequence

<400> 85
ctcgagattt ccccgaaatc tagatttccc cgaaatgatt tccccgaaat gatttccccg 60

aaatatctgc catctcaatt agtcagcaac catagtcccg cccctaactc cgcccatccc 120

gcccctaact ccgcccagtt ccgcccattc tccgccccat ggctgactaa ttttttttat 180

ttatgcagag gccgaggccg cctcggcctc tgagctattc cagaagtagt gaggaggctt 240

ttttggaggc ctaggctttt gcaaaaagct t 271

<210> 86
<211> 32
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> primer useful for generation of a EGR/SEAP reporter construct

<400> 86

gcgctcgagg gatgacagcg atagaacccc gg 32

<210> 87
<211> 31
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> primer useful for generation of a EGR/SEAP reporter construct

<400> 87
gcgaagcttc gcgactcccc ggatccgcct c 31

<210> 88
<211> 12
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_binding
<223> NF-KB binding site

<400> 88
ggggactttc cc 12

<210> 89
<211> 73
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> forward primer useful for generation of a vector containing the NF-KB promoter element

<400> 89
gcggcctcga ggggactttc ccggggactt tccggggact ttccgggact ttccatcctg 60

ccatctcaat tag 73

<210> 90
<211> 256
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_feature
<223> Synthetic NF-KB/SV40 promoter

<400> 90
ctcgagggga ctttcccggg gactttccgg ggactttccg ggactttcca tctgccatct 60

caattagtca gcaaccatag tcccgccccc aactccgccc atcccgcccc taactccgcc 120

cagttccgcc cattctccgc cccatggctg actaattttt tttatttatg cagaggccga 180

UNITED STATES PATENT AND TRADEMARK OFFICE

CERTIFICATE OF CORRECTION

PATENT NO. : 6,994,857 B2
APPLICATION NO. : 09/833041
DATED : February 7, 2006
INVENTOR(S) : DCraig A. Rosen and William A. Haseltine

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

ggccgcctcg gcctctgagc tattccagaa gtagtgagga ggctttttg gaggcctagg 240

ctttgcaaa aagctt 256

--.

In the Claims

Col. 313, line 22, in claim 1 (c), "amino and" should read -- amino --.

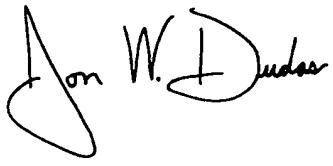
Col. 313, line 33, in claim 1 (e), "or fragment thereof and albumin" should read -- or fragment thereof, and albumin --.

Col. 313, line 55, in claim 1 (i), "proten" should read -- protein --.

Col. 316, line 17, in claim 22, "protein, or thereof" should read -- protein, or fragment thereof --.

Signed and Sealed this

Third Day of October, 2006



JON W. DUDAS
Director of the United States Patent and Trademark Office